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3 **Authentication of commercial candy ingredients using DNA PCR-cloning**
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5 **methodology**
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3 1 **Abstract**
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6 2 **BACKGROUND:** Commercial candies are consumed by all population age sectors
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8 3 worldwide, thus methods for quality control and composition authentication are needed
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10 4 for best compliance of consumer's preferences. In this study the applications of DNA-
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12 5 based methodology for candy quality control have been tested. Eighteen samples of
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14 6 commercial candies (marshmallows, gumdrops, jelly, sherbet, gelatin-based desserts)
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16 7 produced by five countries were analyzed to identify the component species by
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18 8 Polymerase chain reaction, cloning and sequencing of 16S rRNA and ribulose -1,5-
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20 9 diphosphate carboxylase oxygenase genes, and the species determined from BLAST
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22 10 comparison with universal databases and phylogenetic analysis.
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27 11 **RESULTS:** Positive DNA extraction and amplification of the target genes was obtained
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29 12 for 94% of candies assayed, even those containing as little as <0.0005 ng/ μ l DNA
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31 13 concentration. The results demonstrated that the species detected from DNA were
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33 14 compatible with the information provided on candy labels only in a few products. DNA
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35 15 traces of undeclared species, including fish, were found in most samples, and two
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37 16 products were labeled as vegetarian but contained porcine DNA.
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41 17 **CONCLUSION:** Based on the inaccuracy found on the labels of sweets we recommend
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43 18 the use of DNA tests for quality control of these popular sweets. The DNA-tests have
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45 19 been useful in this field but Next Generation Sequencing methods could be more
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47 20 effective.
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53 22 **Keywords:** Candy products, DNA tests, vegetarian labeling, consumer's choice,
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55 23 traceability, labels.
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INTRODUCTION

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26 Candies are consumed worldwide in different cultures and countries.¹ The use of sweets
27 in human diet is very old: ancient Arabian, Chinese and Egyptian peoples consumed
28 candied fruits and nuts cooked with honey, and the Aztecs made a chocolate drink with
29 cocoa seeds.² Now candies are consumed by all population sectors and ages; since they
30 are especially popular for children,^{3,4} their quality control should be a priority.

31 The composition of commercial candies and sweets is complex and often includes many
32 food additives and preservatives.⁵ Many products like soft and jelly-based candy
33 contain gelatin, which is frequently made from pig and cow.^{6,7} The presence of these
34 animals in candy may raise ethical or religious issues in some consumer sectors, for
35 example in vegetarians and in Halal-Kosher consumers,⁷ and consumers should be
36 informed about their choice. Information about the ingredients is important for
37 consumer's health also, since adverse reactions have been reported for allergic patients
38 who consumed candies without knowing they contained saffron,^{8,9} cochineal-made
39 carmine⁹ and peanuts.¹⁰ Anaphylactic shocks after eating marshmallows made from
40 undisclosed fish gelatin have been also documented.¹¹ Therefore, disclosing full
41 information about the species contained in commercial candies is essential for
42 consumers to know what they are eating and help them to make ethical and safe choices.

43 Determining the species composition in commercial candies is not easy because they are
44 generally highly processed and can contain a mixture of products. DNA has been often
45 used for determining species composition in food, and nowadays the techniques for
46 DNA extraction and amplification by Polymerase chain reaction (PCR) allow the
47 successful analysis of highly processed products,¹²⁻¹⁵ detecting even small traces.¹⁶ In
48 the present study we have purchased different types of candies produced by five

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3 49 countries, for determining their species composition employing DNA-based molecular
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5 50 techniques. Two different primer sets specific for animal or plant species were
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7 51 employed for PCR amplification and cloning of DNA extracted from the candies. From
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9 52 the results we have assessed the utility of this DNA-based methodology for quality
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11 53 control in candy markets. The following parameters were considered for the assessment:
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13 54 DNA content, PCR-amplification success, number of species detected, accuracy of
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15 55 species identification (from concordance of two assignment methods, BLAST-based
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17 56 and phylogenetic). In addition, comparing the detected and declared species we have
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19 57 evaluated the accuracy of current candy labelling to recommend improvements in
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21 58 quality control, if needed.
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26 **EXPERIMENTAL**

27 28 29 **Sampling**

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32 61 Eighteen candies from five countries: Spain (8 samples), France (2 samples), Portugal
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34 62 (4 samples), Sweden (1 sample), Spain/Portugal (2 samples), Spain/Turkey (1 sample)
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36 63 were analyzed (Table 1). Different products were considered (Fig. 1), including raw
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38 64 gelatin powder (3), desserts (3), soft candies (7), marshmallows (2), gums (2) and
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40 65 sherbet powder (1). The information provided in each candy label was analyzed in
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42 66 detail, especially the list of ingredients, allergy warnings and indications for specific
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44 67 consumer sectors such as vegetarians, vegans and persons with food restrictions.
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48 **DNA extraction, quantification, PCR amplification and sequencing process**

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51 69 DNA analysis was carried out in strict sterile conditions to prevent contamination, and
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53 70 both pre- and post-PCR processes were controlled. Sample manipulation was done
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55 71 within a sterile room cleaned with 100% ethanol and 10% bleach. All the material
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57 72 employed was cleaned and put in sterile bags to autoclaving. DNA extraction and PCR
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3 73 amplification were performed into a flow chamber within that sterilized room, with
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5 74 ultraviolet light to ensure destruction of any possible contaminant DNA. During all the
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7 75 process researchers wore two pairs of gloves, paper mask and cap and laboratory coat.
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9 76 Negative controls were used to check possible contamination during the laboratory
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11 77 analysis, from the DNA extraction process to the visualization of PCR products in
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13 78 agarose gels. Pig (*Sus scrofa*) and rainbow trout (*Oncorhynchus mykiss*) were used as
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15 79 positive controls of animal detection with the 16S rRNA gene, and apple (*Malus*
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17 80 *domestica*) was the positive control for plant detection with rbcL gene. For the rest of
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19 81 post-PCR processes we worked in other laboratory within another flow chamber, also
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21 82 under ultraviolet light.
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26 83 DNA extraction was performed with the kit DNeasy Mericon Food Kit of QIAGEN.
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28 84 From each candy four Eppendorf tubes with 200 mg each one were employed for DNA
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30 85 extraction to get more amount of DNA. Two cleaning steps were done to eliminate
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32 86 potential inhibitors of polymerase chain reaction: first with CTAB detergent and second
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34 87 with chloroform. After, the contents from the four tubes of the same candy was put
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36 88 together to continue with the rest of the protocol. DNA was quantified using Qubit
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38 89 dsDNA HS Assay Kit in a Qubit 2.0 Fluorometer. The detection limit of this method is
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40 90 0.0005ng/μl.
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45 91 PCR amplification was done with the kit PCR core Kit Plus of Roche, with the enzyme
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47 92 uracil glycosylase and dideoxynucleotide with uracil instead of thymine. Since candies
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49 93 are highly processed their DNA is likely degraded,¹⁷ therefore we targeted short
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51 94 species-specific sequences. For animal species we employed the primers 16S-HF 5'-
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53 95 ATAACACGAGAAGACCCT-3' and 16S-HR 5'-CCCRCGGTCGCCCAAC-3'
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55 96 developed by Horreo *et al.*¹⁸ that amplify an 80-122 base pair (bp) fragment within the
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57 97 16S rRNA gene. PCR reaction was performed with: 5 μl of DNA extraction from the
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3 98 candy (from less than 0.0005 ng/ μ l to 0.328 ng/ μ l), 0.125 μ l of Taq polymerase from the
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5 99 PCR core Kit Plus of Roche, polymerase solution with Mg²⁺ 1x, 0.5 μ l of each primer
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7 100 10 μ M, 0.5 μ l dideoxynucleotides (dNTPs with U), 0.5 μ l of Uracil glycosylase and bi-
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9 101 distilled water up to 25 μ l of total volume. The PCR conditions were: a cycle at 20 °C
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11 102 for 5 min and at 95°C for 2 min to activate and deactivate the uracil glycosylase enzyme
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13 103 respectively; then, 40 cycles at 95°C for 30s, 55°C 30s, 72°C 1min 30s, and a final cycle
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15 104 at 72°C during 7 min. For plant species we employed the primers Plant159-F
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17 105 CTTGATTTTACCAAAGATGATGA and Plant159-R
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19 106 TTCTTCGCATGTACCCGCAG designed by Han *et al.*¹⁹ for amplifying a 159 bp
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21 107 fragment of the ribulose-1,5-diphosphate carboxylase oxygenase gene (rbcL). PCR
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23 108 reaction was performed in the same way than 16S rDNA gene but the PCR conditions
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25 109 after the cycle for uracil glycosylase enzyme were 50 cycles at 95°C for 30s, 58°C 30s,
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27 110 72°C 1min 30s, and a final cycle at 72°C during 7 min.
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32 111 PCR products were run in 2% agarose gels stained with ethidium bromide. Purification
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34 112 of PCR product was performed with IllustraIM ExostarIM 1-Step de GE Healthcare
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36 113 Life Sciences. Direct sequencing was performed at the sequencing facilities of the
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38 114 University of Oviedo employing BigDye Terminator Cycle Sequencing chemistry and
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40 115 ABI Prism 3130xl Genetic Analyzer. Chromatograms evidenced species mixture, thus
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42 116 cloning approaches were employed to obtain individual sequences. After purification of
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44 117 PCR product with Wizard SV Gel and PCR Clean-Up System Kit (Promega), the
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46 118 purified DNA was cloned using the Dual Promoter TA Cloning Kit (Invitrogen), with
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48 119 pCR II vector and competent cells TOP10'. Briefly, we did the ligation and performed a
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50 120 transformation process by thermal shock. Then the bacteria (*Escherichia coli*) were
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52 121 grown in liquid SOC medium for 1 hour and spread on solid LB medium with
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54 122 ampicillin. When bacteria grew (only bacteria carrying the vector are ampicillin-

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3 123 resistant) we picked white colonies, which carry the insert (their β -galactosidase gene is
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5 124 interrupted) in 50 μ l of bidistilled water. DNA was extracted from the colonies by
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7 125 thermal shock at 95 °C during 5 min and a PCR was performed using the primers T7
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9 126 and SP6 located in the flanking regions of the insertion site. The reaction mix of this
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11 127 PCR was: 1.5 units of Taq polymerase of Biotools (5U/ μ l), polymerase solution 1x, 1.5
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13 128 mM of Mg²⁺, 1 μ l of each primer 10 μ M, dideoxynucleotides (dNTPs) of 2.5 mM and
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15 129 bidistilled water up to 20 μ l of total volume. PCR conditions were: a cycle at 95°C for 5
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17 130 min; 35 cycles at 95°C for 30s, 55°C 30s, 72°C 30s, and a final cycle at 72°C during 10
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19 131 min. Purification and sequencing were made as explained above.
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24 132 **Analyses of sequences**

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27 133 The sequences obtained were edited using BioEdit program²⁰ and compared with
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29 134 GenBank database (www.ncbi.nlm.nih.gov/genbank/) using BLAST Nucleotide tool
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31 135 (nBLAST). Species assignment was done to the best match reference sequence within
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33 136 GenBank. Species assignation was confirmed from phylogenetic methodology. A
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35 137 Neighbor-Joining tree containing the problem sequences and reference sequences from
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37 138 GenBank was reconstructed with MEGA version 6,²¹ with Tamura Nei model²² and
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39 139 uniform substitution rates. Robustness of the Neighbor-Joining topology was assessed
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41 140 using 10,000 bootstrap replicates.
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45 141 **RESULTS**

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48 142 DNA yields obtained from the analyzed candies ranged between undetectable
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50 143 <0.0005ng/ μ l in seven products (samples #3, #7, #8, #10, #15, #17 and #18) to
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52 144 0.328ng/ μ l in the Portuguese gelatin of sample#6 (Table 1). Positive PCR amplification
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54 145 of one or the two assayed markers occurred from all except one product, fish gummies
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3 146 (sample#3, Table 1). This means that DNA was present at least in 17 out of 18 samples
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5 147 (94.4%), although in very low (undetectable) quantity in six of them.
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8 148 In the cases of successful DNA amplification, clean negative controls were obtained in
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10 149 all PCR (e.g., Fig. 2). The number of sequences retrieved in total from the 17 candies
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12 150 with positive PCR amplification was 118 for the 16S rDNA gene and 94 for the rbcL
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14 151 gene. The sequences were submitted to the European Nucleotide Archive (ENA), from
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16 152 the European Bioinformatics Institute in the European Molecular Biology Laboratory,
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18 153 EMBL-EBI (www.ebi.ac.uk/). Their accession numbers are HG964177-HG964248. For
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20 154 the 16S rRNA gene, amplicons ranged 116-122 bp in length and exhibited nucleotide
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22 155 polymorphisms corresponding to 13 haplotypes that allowed to unambiguously
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24 156 identifying five animal species to species level: cow *Bos taurus*, pig *Sus scrofa*, chicken
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26 157 *Gallus gallus*, deep Cape hake *Merluccius paradoxus*, human *Homo sapiens*. One
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28 158 haplotype could be assigned only at genus level (hake *Merluccius* sp.). For the rbcL
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30 159 gene, 159 bp long amplicons were obtained representing 14 haplotypes. Seven species
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32 160 were unambiguously identified from the haplotypes found for this DNA region: maize
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34 161 *Zea mays*, soya *Glicine max*, cacao *Theobroma cacao*, onion *Allium cepa*, tobacco
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36 162 *Nicotiana tabacum* and chestnut *Castanea sativa*. One haplotype exhibited the same E-
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38 163 value for two match hits with references sequences of wheat (*Triticum* sp.) and rye
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40 164 (*Secale cereale*), of the family Poaceae, and another with cumin (*Cuminum cyminum*)
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42 165 and carrot (*Daucus carota*), of the family Apiaceae. The remaining haplotypes could
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44 166 taxonomically assign the sequences only at genus (beans, *Vicia* sp.; rice, *Oryza* sp.;
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46 167 honeybush, *Ciclopia* sp.) or family level (Oleaceae). In spite of the short length of the
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48 168 two sequences here employed, the reconstructed Neighbor-Joining trees exhibited a
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50 169 rather good phylogenetic signal, grouping together the haplotypes of the same species or
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52 170 genus in the tree reconstructed from 16S rDNA sequences (Fig. 3). Likewise, the tree
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3 171 reconstructed from rbcL sequences clustered haplotypes by family (Fig. 4); however,
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5 172 and as expected from their shorter length, bootstrapping values were lower than in the
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7 173 16S rDNA-based tree, and some phylogenetic discrepancies occurred; for example, the
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9 174 sequences identified as *A. cepa* (onion), expected to be clustered with other Liliopsida
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11 175 such as the cereals, were alone in a branch apart.

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14 176 Regarding candies composition, from 16S rDNA one animal species was found for most
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16 177 samples (Table 2), pig (*S. scrofa*) being the most frequent (in 64.7% of candies)
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18 178 followed by cow (*B. taurus*) (47.1% of candies), hake (genus *Merluccius*) (11.8%) and
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20 179 chicken (*G. gallus*) (5.5%). From rbcL sequences (Table 2) a mixture of at least three
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22 180 plant species was detected in eight of the samples analyzed (44.4%). Seven samples
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24 181 contained maize (*Z. mays*) and also seven samples contained beans or related species
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26 182 (*Vicia* sp.). Less frequent ingredients were cereals of the tribe of wheat/rye; soya, rice,
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28 183 honeybush and chestnut; tobacco, cacao, cumin and Oleaceae (found from five; two;
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30 184 and one samples respectively). Some ingredients were unexpected, since contamination
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32 185 from the analysis process can be discarded given clean negative PCR controls and strict
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34 186 measures of sterility, such as human DNA and tobacco found in eight (44% samples:
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36 187 #2, #7, #8, #11, #13, #14, #15 and #17) and one (#13) candies respectively (Table 2).

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39 188 Many species detected from DNA were not stated in the labels and vice versa (Table 2).
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41 189 Only one of the samples analyzed provided DNA results concordant with the label: the
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43 190 gelatin powder of Sample#1 (Tables 1 and 2) that declared to contain porcine gelatin
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45 191 and contained porcine DNA. Other DNA-label concordances occurred in a few samples:
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47 192 #11 label also declared porcine gelatin and porcine DNA was found; #2 and #7 declared
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49 193 corn and contained corn DNA, as did occur in #8 for soya and #15 for wheat. In general
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51 194 there was a difference between the means of animal and plant species found only from
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53 195 DNA and only from labels (Fig. 5, Table 2). More animal species were found from
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3 196 DNA than from labels with Horreo *et al.*¹⁸ primers, whereas for plants it was the
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5 197 opposite, with more plants and fruits stated in the labels than found from DNA with
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7 198 Han *et al.*¹⁹ primers.
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10 199 Some cases found in this study can be problematic for consumers. Pig, not accepted by
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12 200 some religions, is one example. Pig traces appeared but were not declared in 55.6% of
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14 201 samples (Fig. 4). Moreover, two samples labeled as apt for vegetarians (vanilla custard,
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16 202 Sample#2; agar, Sample#5) contained pig traces. Another possible problematic case
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18 203 was the failure to declare fish content, although hake traces were present in three
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20 204 samples.
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24 205 **DISCUSSION**

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27 206 Our results revealed that DNA traces were present in most analyzed commercial
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29 207 candies, and that its quality and concentration was sufficient for successful PCR
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31 208 amplification of short DNA sequences of species-specific value. The results obtained
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33 209 here confirm the power of DNA tests for detecting traces of ingredients in complex food
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35 210 matrices, supporting other authors who used DNA for identifying unwanted species in
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37 211 candy, for instance Demirhan *et al.*⁷ Most studies use specific markers for identifying
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39 212 only targeted species or DNA sequences; for example the mentioned study targeting
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41 213 porcine,⁷ markers for detecting genetically modified maize and soy,¹² or saffron in
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43 214 highly processed products.¹⁵ Here we have followed a different approach of PCR-
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45 215 cloning of conserved DNA sequences using universal primers, instead of species-
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47 216 targeted ones, because our objective was to detect as many species as possible. Indeed,
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49 217 not finding a species in only a dozen sequences (from cloning) cannot ensure that such
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51 218 species is absent from the product; it could be present in low proportion and remain
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53 219 undetected. Due to the many ingredients contained in candy, this process could be
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3 220 considerably improved using next generation sequencing technology (NGST): high-
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5 221 throughput sequencing approaches after direct DNA extraction from a matrix or
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7 222 environmental sample. Capable to generate millions of sequences at the same time,
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10 223 NGST is now used in ecology for biodiversity monitoring, and its application in food
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12 224 sciences has been suggested for microbes in complex food matrices.^{23,24}
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15 225 It should be taken into account that the absence of DNA traces of a species in a
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17 226 product does not imply that species is really absent; DNA can be so degraded that PCR
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19 227 may fail, and/or primers may fail to anneal if they are insufficiently specific for a
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21 228 taxonomic group. Conversely, if DNA traces of a species occur in a product and
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23 229 contamination can be reasonably discarded, as it is the present case, there is no doubt
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25 230 that the species is really present in that product. Despite quite limited sample size, in our
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27 231 results we found a surprising and unexpected high level of failure to declare species
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29 232 contents in commercial packed candies. Many undeclared species were detected in more
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31 233 than 90% of the analyzed candies, and some of them could raise ethical issues (pig;
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33 234 animal species in vegetarian candies) for many consumers. Since the candy trade is
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35 235 widely globalized,²⁵ and our study was done from candies made in five different
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37 236 countries, the results here obtained could likely be generalized.
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42 237 Regulations of candy labelling are not homogeneous worldwide and each country has
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44 238 specific laws, generally focused on allergenic ingredients. For example, in the US it is
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46 239 mandatory to list major allergens contained in the ingredients on the label of packed
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48 240 food, including candy, stating the species the major allergen is derived from (Food
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50 241 Allergen Labelling and Consumer Protection Act of 2004; Public Law 108-282, Title
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52 242 II). In European common law, packed food must also display a list of potential allergens
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54 243 separated from the list of ingredients (EU 1169/2011). In addition to this general
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56 244 normative, at national level some regulations are specifically applied to candy; for
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3 245 example, in Spain the Royal Decree 1245/2008 states that packed candies must exhibit
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5 246 information about allergens on the label. The results of the present study suggest that
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7 247 the current labeling normative should be improved. At least the species used for the
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9 248 gelatin should be disclosed. The consumer should be informed about fish, which can
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11 249 trigger allergic reactions if inadvertently eaten with candy.¹¹ On the other hand, pig and
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13 250 cow are frequently employed to produce commercial gelatin,^{6,7} thus their presence in
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15 251 most candies here analyzed is not surprising. However, their occurrence in candies
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17 252 labelled “For vegetarians” could be considered a fraud and undermine the choice rights
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19 253 of vegetarian consumers.
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23 254 The causes of failure for declaring all the species detected in this study are probably
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25 255 diverse. Some ingredients could have been merely listed as "colorants" or "spice",
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27 256 without disclosing the species contained.²⁶ In some cases it could be likely deliberate,
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29 257 as in Sample#5 supposedly made only from algae (colorants were not stated) but
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31 258 containing really pig, bean and honeybush traces. However in other cases the presence
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33 259 of some traces could be inadvertent. Some ingredients could have been accidentally
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35 260 acquired during the process of packing.²⁷ This could happen also in the cases of
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37 261 contamination with human DNA and even tobacco; it is very difficult to imagine that
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39 262 negligent manipulation of food products is deliberate. However, although likely not
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41 263 deliberate in some (perhaps in many) cases, the results found our study strongly support
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43 264 the need of a more careful control of the international candy market.
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48 49 265 **CONCLUSIONS**

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52 266 Using DNA analysis we have detected a generalized failure to inform about ingredients
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54 267 in commercial candies from five producer countries. DNA traces of many species
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56 268 undeclared in the labels like porcine, fish, soya, honeybush and others were found from
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3 269 most analyzed samples. Undeclared porcine DNA was found in samples labeled as “For
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5 270 vegetarians”, undermining the rights of vegetarian consumers. A more strict control of
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7 271 commercial candies is recommended, applying methodology based on DNA-tests or
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9 272 Next Generation Sequencing Technology, which could obtain higher resolution on the
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11 273 composition of these sweets.
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28 280 European Bioinformatics Institute in the European Molecular Biology Laboratory,
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30 281 EMBL-EBI (<http://www.ebi.ac.uk/>). We also acknowledge the assistance of Daniel
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TABLES

Table 1: summary of candy samples analyzed.

S	Country	Type	Animal species	Plant species	Specific indications	DNA (ng/μl)	PCR amplification	
							16S rDNA	rbcL
1	Spain/Portugal	Unflavored gelatin	Pork	No	ND	0.0384	+	-
2	France	Vanilla custard	ND	Maize	Vegetarian	0.172	+	+
3	Spain	Fish-shaped gummies	Possible milk, egg traces	Possible peanuts, tree nuts, wheat, soy traces	ND	<0.0005	-	-
4	France	Lemon gelatin dessert	Gelatin. Possible milk & egg traces	Possible soy, nuts traces	Possible gluten content	0.0124	+	+
5	Spain/Portugal	Vegetable gelatin	ND	Agar-agar	Vegan, Agar 100%	0.0258	+	+
6	Portugal	Neutral gelatin	Gelatin	ND	ND	0.328	-	+
7	Spain	Marshmallows	Gelatin	Corn; Arabic gum	Gluten-free	<0.0005	+	+

8	Spain	Strawberry bubble gum	ND	Soya, arabic gum	ND	<0.0005	+	+
9	Spain	Strawberry candy	Gelatin, cochineal	Cherry, lemon, pineapple, strawberry, orange, apple, blackcurrant, elder berry, aronia, grape, mango, passion fruit, carob, turmeric	ND	0.0238	+	-
10	Portugal	Watermelon candy	Gelatin	ND	ND	<0.0005	+	+
11	Portugal	Marshmallows	Porcine gelatin	Wheat, corn	ND	0.0226	+	+
12	Spain	Green soft jelly	ND	Lemon, orange, strawberry, apple, pineapple, safflower, potato, carrot, radish, hibiscus, blackcurrant, spirulina.	Gluten free	0.0484	+	+
13	Spain	Color gummies	Gelatin	Carrot, blackcurrant, paprika, turmeric	ND	0.0164	+	+
14	Sweden	Gummies	Gelatin	Licorice, peanuts	ND	0.0174	+	+

15	Portugal	Pineapple gelatin dessert	Gelatin; Possible eggs & milk traces	Possible wheat traces	ND	<0.0005	+	+
16	Spain	Strawberry candy	Gelatin, cochineal	Cherry, lemon, pineapple, strawberry, orange, apple, blackcurrant, elder berry, aronia, grape, mango, passion fruit, carob, turmeric	ND	0.0208	+	+
17	Spain	Sherbet powder	ND	ND	Sugar & flavours	<0.0005	+	-
18	Turkey/Spain	Fruit bubble gum	Gelatin	Watermelon, pineapple, melon, arabic gum, turmeric	Contains Brilliant Blue FCF	<0.0005	+	+

Country of origin, type of product, animal and plant species declared in the label, specific indications for consumers, DNA quantity determined by fluorometry, PCR amplification of the markers assayed (positive or negative as visualized in agarose gel).

Table 2: Composition of the analyzed candy samples as identified from DNA.

Sample	N° species		Clones	Cow	Pork	Hake	Chicken	Beans	Rice	Cereals	Apiaceae	Oleaceae	Onion	Chestnut	Honeybush	Soya	Cacao	Corn	Contaminants
	Animals	Plants																	
1	1 (1)	0 (0)	8	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2 (veg)	1 (0)	2 (1)	11	-	+	-	-	-	-	+	-	-	-	-	-	-	-	+	+
3	0 (2)	0 (4)	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4	2 (3)	4 (2)	14	+	+	-	-	+	-	+	-	-	+	-	-	-	+	-	-
5 (veg)	1 (0)	2 (1)	12	-	+	-	-	+	-	-	-	-	-	-	+	-	-	-	-
6	0 (1)	3 (0)	6	-	-	-	-	+	+	-	+	-	-	-	-	-	-	-	-
7	4 (1)	1 (2)	16	+	+	+	+	-	-	-	-	-	-	-	-	-	-	+	+
8	3 (0)	2 (2)	10	+	+	+	-	+	-	-	-	-	-	-	-	+	-	-	+
9	1 (2)	0 (14)	5	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

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10	1 (1)	3 (0)	13	+	-	-	-	+	-	+	-	-	-	-	-	-	+	-
11	1 (1)	0 (2)	8	-	+	-	-	-	-	-	-	-	-	-	-	-	-	+
12	1 (0)	3 (12)	17	+	-	-	-	+	-	-	-	+	-	-	+	-	-	-
13	2 (1)	2 (4)	14	+	+	-	-	+	-	-	-	-	-	-	-	-	+	+
14	2 (1)	3 (2)	15	+	+	-	-	-	-	+	-	-	-	-	-	+	-	+
15	2 (3)	2 (1)	17	-	+	+	-	-	+	+	-	-	-	-	-	-	-	+
16	1 (2)	3 (14)	19	+	-	-	-	-	-	+	-	-	-	+	-	-	-	-
17	1 (0)	0 (0)	4	-	+	-	-	-	-	-	-	-	-	-	-	-	-	+
18	1 (1)	3 (5)	23	-	+	-	-	-	-	-	-	-	-	+	+	-	-	+

Number of animal and plant species from DNA (declared in the label in parenthesis); number of clone sequences obtained from each sample; presence/absence of different ingredients authenticated from DNA sequences as +/- . Samples indicated for vegetarians are marked with (veg)

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For Peer Review

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3 1 LEGENDS OF FIGURES
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6 2 Figure 1: Photographs of different samples of this study: (1) Sample#1, gelatin powder
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8 3 (2) Sample#3, fish gummy; (3) Sample#2, pre-cooked mix for vanilla custard (4);
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10 4 Sample#4, lemon jelly; (5) Sample#8, strawberry gum; (6) Sample#7, marshmallow; (7)
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12 5 Sample#9, strawberry candy; (8) Sample#10, watermelon jelly; (9) Sample#12, green
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14 6 candy; (10) Sample#18, fruit gum; (11) Sample#11, marshmallow; (12) Sample#14,
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16 7 candy; (13) Sample#13, soft candy.
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20 8 Figure 2: Photography of 2% agarose gel stained with ethidium bromide and visualized
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22 9 under UV light showing PCR products obtained with the 16S-H (A) and Rbc-L (B)
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24 10 primers; from left to right in A gel: positive control, samples 8-11 (two lanes/sample),
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26 11 negative control, empty lane, DNA ladder (marker of size, in base pairs); B gel: samples
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28 12 8-11 (two lanes/sample), positive control, DNA ladder and negative control.
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32 13 Figure 3: Neighbor-Joining tree reconstructed from the 16S rDNA sequences obtained
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34 14 from the analyzed candy. The haplotype name is followed by the closest taxonomic
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36 15 match. Reference sequences are included indicated as ref_ with their GenBank
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38 16 accession number. A sequence of the limpet *Patella depressa* was employed as
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40 17 outgroup.
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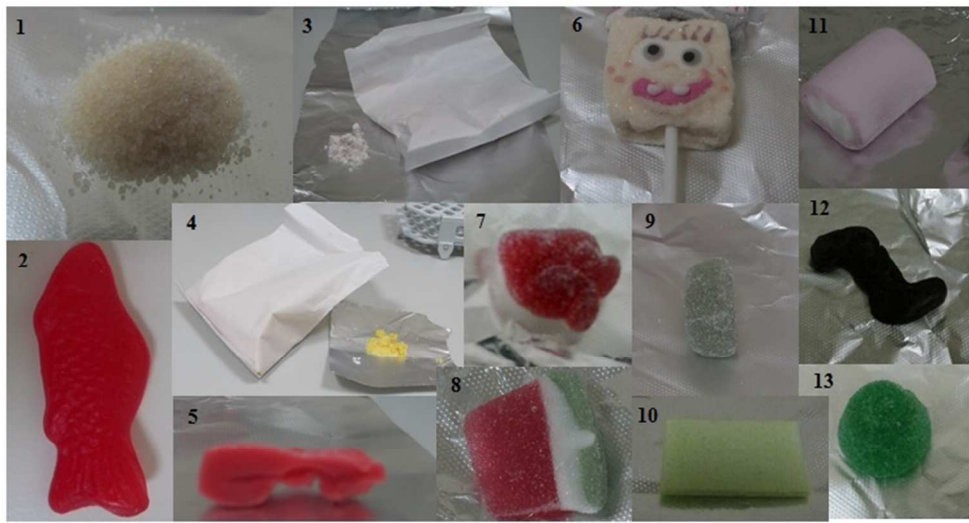
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44 18 Figure 4. Neighbor-Joining tree reconstructed from the rbcL sequences obtained from
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46 19 the analyzed candy. The haplotype name is followed by the closest taxonomic match.
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48 20 Reference sequences are included indicated as ref_ with their GenBank accession
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50 21 number. A sequence of the green alga *Fucus vesiculosus* was employed as outgroup.
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54 22 Figure 5: Mean number per candy sample of animal and plant species of the following
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56 23 types: concordant, declared only in the labels and found only from DNA.
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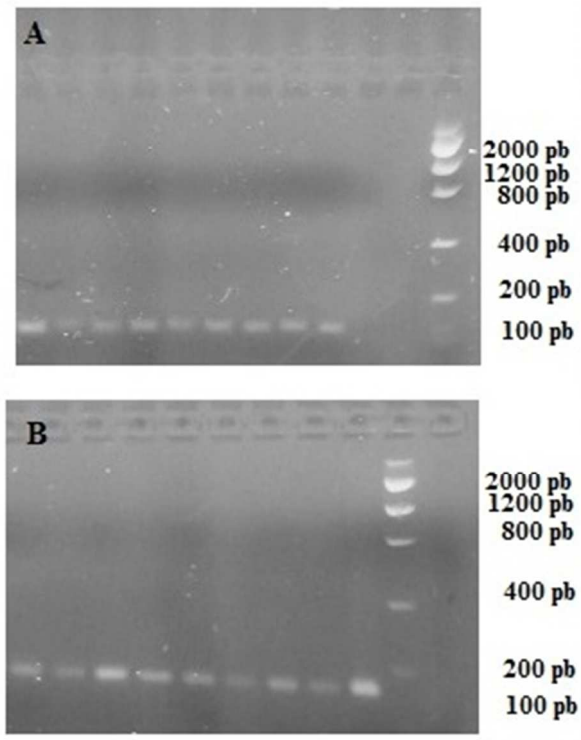
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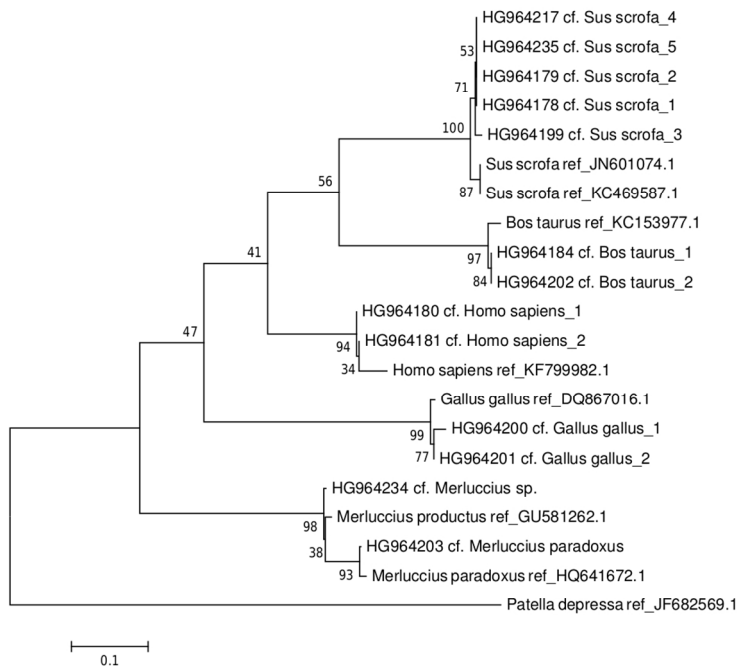
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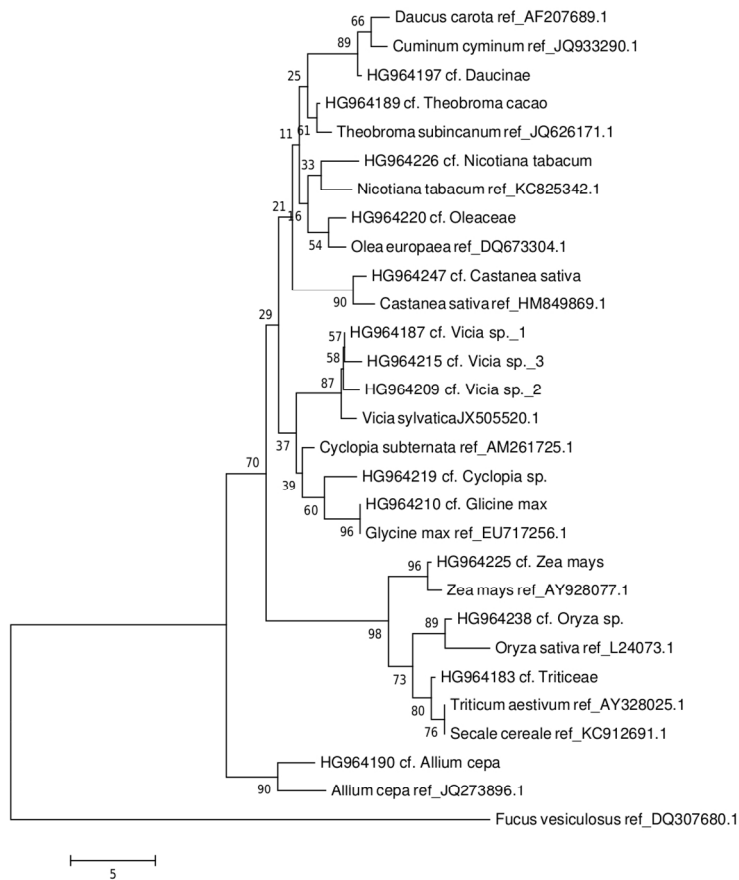
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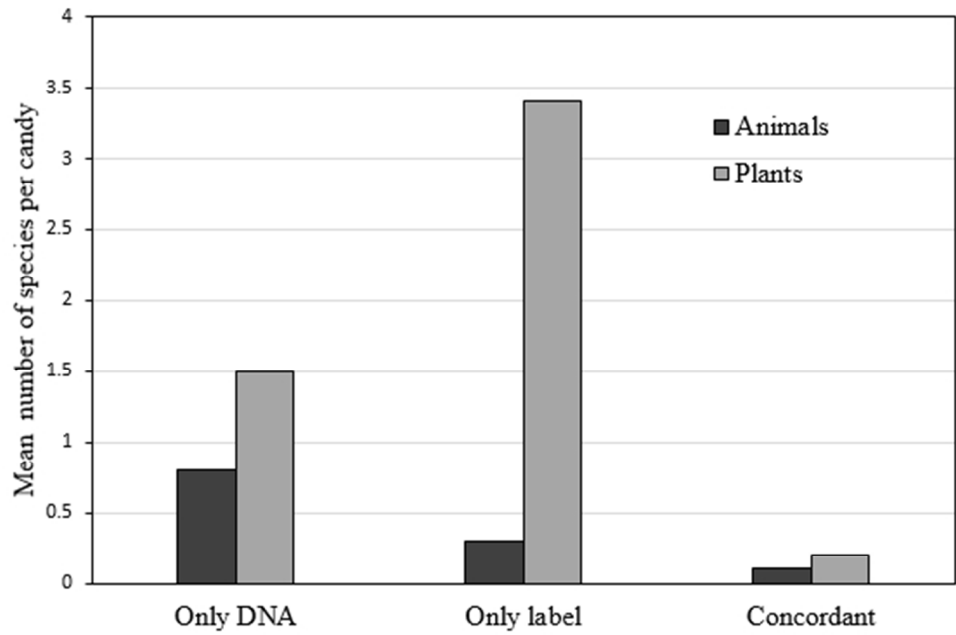


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